Please amend the paragraph beginning on page 39, line 24, through page 40, line 5, as follows:

EXAMPLE 2

LEAD OPTIMIZATION BY RECEPTOR-BASED FREE ENERGY QUANTIATIVE STRUCTURE ACTIVITY RELATIONSHIPS (QSARS) FOR TUMOR NECROSIS *factor* [TNF](TNF) RECEPTOR ANTAGONIST FINDING

The goal of the modeling studies in this phase was to discover the binding modes and complex structures of the compounds that bind to TNF receptor type I protein, in order to guide design of new compounds. An approach that relies on docking compounds to the receptor, evaluating free energy changes of binding of the docked structures, and comparing the calculated values with experimental inhibition constants K_i of the compounds was developed. The success of the calculations was [evalulated]evaluated by the consistency of the calculated free energy changes of binding and the experimental K_i.

IN THE ABSTRACT:

Please amend the abstract as follows:

Please amend the paragraph on page 51, lines 1-12, as follows:

ABSTRACT OF THE DISCLOSURE

Provided herein are computer-based methods for generating and using three-dimensional (3-D) structural models of target biomolecules. In particular, the target biomolecules are protein structural variants derived [yfrom]from genes containing genetic variations, or polymorphisms. The models are generated using molecular modeling techniques, such as homology modeling. The models can be used in structure-based drug design studies to identify drugs that bind to particular structural variants in structure-based drug design studies, for designing allele-specific drugs, population-specific drugs and for predicting clinical responses in patients. Molecular structure databases containing protein structural variant models are also provided.